

**Table S1. Overview of the 186 (non-) CPPs, including their CP-response.**

Peptide ID	Peptide name	Sequence	Number of AA	CP-response	Ref.
1	pVEC	LLIILRRRIRKQAHHSK	18	1.318	17, 25, 27, 53, 66
2	Tat 48-60	GRKKRRQRRRPPQ	13	0.221	17, 26, 34, 38, 66
3	APH-1 (85-98)	VFRFAYYKLLKKA	13	0.188	26
4	APH-1 (236-246)	LRSIQRSLCK	11	0.039	26
5	Nicastrin (38-53)	RKIYIPLNKTAPCVR	15	0.345	26
6	Nicastrin (414-434)	RRPNQSQPLPSSLRFLRAR	21	0.016	26
7	Nicastrin (616-635)	RLPRCVRSTARLARALSPAF	20	0.031	26
8	Presenilin-1 (97-109)	VATIKSVSFYTRK	13	0.008	26
9	Presenilin-1 (305-317)	AQRRVSKNSKYNA	13	0.016	26
10	D-pVEC	llilrrrirkqahahsk	18	0.824	7, 27, 53
11	(KFF) <sub>3</sub> K	KFFKFFKFFK	10	1.837	27
12	Transportan	GWTLNSAGYLLGKINLKALAALAKKIL	27	(4.357)	17, 28, 68
13	Transportan 10	AGYLLGKINLKALAALAKKIL	21	1.641	28, 30, 32, 34, 66
14	MAP	KLALKLALKALKAALKLA	18	1.716	13, 17, 29, 37, 53
15	Syn B1	RGGRLSYSRRRFSTSTGR	18	0.063	17, 39
16	Polyomavirus Vp <sub>1</sub>	APKRKSGVSK	10	0.028	17
17	Bac1-15	RRIRPRPRLPRPRP	15	0.035	17
18	NF-κB	VQRKRQKLMP	10	0.025	17
19	SV40-T antigen	PKKKRKV	7	0.028	17
20	HATF <sub>3</sub>	ERKKRRRE	8	0.023	17
21	hCT(9-32)	LGTYTQDFNKFHTFPQTAIGVGAP	24	0.024	17
22	HIV-1 Rev (34-50)	TRQARRNRRRRWRERQR	17	1.460	17, 38, 56
23	Integrin	VTVLALGALAGVGVG	15	0.549	17
24	DPV6	GRPRESGKKRKRRLKP	17	0.073	17
25	S4 <sub>13</sub> PV	ALWKTLLKKVLKAPKKRKRK	20	0.781	17
26	Pep-1	KETWWETWWTEWSQPKKKRKRK	21	0.105	17
27	MPG	GALFLGWLGAAGSTMGAWSQPKKKRKRK	27	1.065	17
28	Poly-P (SAP)	VRLPPVLRPPPVLRRPPP	18	0.027	17
29	R7	RRRRRRR	7	0.395	12, 16, 17, 36
30	R9	RRRRRRRRR	9	1.000	17, 31, 33, 41, 42, 47, 63
31	pVEC scrambled	IAARIKLSRQHIKLRHL	18	0.101	7, 17
32	Tat 47-57	YGRKKRRQRRR	11	0.309	30, 33, 42, 58
33	Tat 48-59	GRKKRRQRRRPP	12	0.192	31, 63
34	M918	MVTVLFRRLRIRACGPPRVV	22	(7.158)	32
35	Penetratin	RQIKIWFQNRMMKWKK	16	1.000	33, 39, 44
36	R11	RRRRRRRRRR	11	0.211	34
37	RL9	RRLRLRLR	9	0.134	35
38	RW9	RRWRRWR	9	1.301	35
39	R7W	RRRRRRRW	8	1.687	36
40	VP22	NAKTRRHERRRKLAIER	17	0.161	38
41	D-Syn B1	rggrlsysrrrfststgr	18	0.089	39
42	Syn B3	RRLSYSRRRF	10	0.126	39
43	D-Syn B3	rrlsysrrrf	10	0.185	39
44	Syn B5	RGGRLAYLRRRWAVLGR	17	1.159	39
45	ARF (1-22)	MVRRFLVTLRIRACGPPRVV	22	1.641	40
46	ARF (1-22) scrambled	FVTRGCPRLVRLIRVMVPRR	22	1.296	40
47	ARF (2-14)	VRRFLVTLRIRRA	13	0.950	40
48	ARF (2-14) scrambled	RVRILARFLRTRV	13	0.173	40
49	ARF (19-31)	RVRVFVHIPRLT	13	1.382	40
50	ARF (19-31) scrambled	VIRVHFRLPVRTV	13	0.259	40
51	hLF	KCFQWQRNMRKVRGPPVSCIQR (disulfide 2-19)	22	0.952	41
52	MAP (II)	KALAALLKLLAKLLAALK	18	0.181	13
53	MAP (III)	KLALKLALKALKAALK	16	0.115	13
54	MAP (VII)	KLALKLALKALQAALQLA	18	0.022	13
55	MAP (VIII)	KLALQLALQALQAALQLA	18	0.243	13

56	MAP (XI)	LKTLATALTKLAKLTTL	18	0.177	13
57	MAP (XIII)	LKTLTETLKELTTEL	18	0.052	13
58	MAP (XV)	RQKIWFQNRMRKWK	16	0.104	13
59	KLA 1	KLALKLALKAWKAAKLA	18	0.085	13
60	KLA 2	KLALKAALKAWKAAKLA	18	0.008	13
61	KLA 11	KITLKLAIKAWKLALKAA	18	0.025	13
62	KLA 5	KIAAKSIKIWSILKIA	18	0.036	13
63	KLA 12	KALAKALAKLWKALAKAA	18	0.079	13
64	KLA 13	KLALKLALKWAKLALKAA	18	0.008	13
65	KLA 14	KLLAKAARKWLLALKAA	18	0.015	13
66	KLA 9	KLLAKAALKWLLKALKAA	18	0.023	13
67	KLA 10	KALKKLLAKWLAALKALL	18	0.115	13
68	KLA 15	KLAAALLKKWKKLAAALL	18	0.120	13
69	KLA 8	KALAALLKKWAKLLAALK	18	0.181	13
70	TP10-1	AGYLLGPNLAKALAALAKKIL	21	1.223	11
71	TP10-2	AGYLLGKINLPLAALAKKIL	21	0.749	11
72	TP10-3	AAYLLAKINLAKALAALAKKIL	21	1.243	11
73	TP10-4	AGYLLGKINLRALAALARRIL	21	1.263	11
74	TP10-5	AGYLLGKINLKKLAKL(Aib)KKIL <sup>1</sup>	21	2.141	11
75	D-R9	rrrrrrrr	9	1.389	12, 43
76	MP	INLKALAALAKKIL	14	0.570	45
77	iMP	inlkalaalakkil	14	(3.602)	45
78	rMP	LIKKALAALAKLNI	14	0.352	45
79	riMP	likkalaalaklni	14	0.288	45
80	MitP	INLKKLAKL(Aib)KKIL <sup>1</sup>	14	2.712	45, 46
81	iMitP	inlkklakl(Aib)kkil	14	2.272	45
82	rMitP	LIKK(Aib)LKALKKLNi	14	0.531	45
83	riMitP	likk(Aib)lkalkklni <sup>1</sup>	14	0.837	45
84	Cyt c <sup>77-101</sup>	GTKMIFVGIKKKEERADLIAYLKKA	25	0.179	46
85	Cyt c <sup>86-101</sup>	KKKEERADLIAYLKKA	16	0.006	46
86	Cyt c <sup>79-92</sup>	KMIFVGIKKKEERA	14	0.013	46
87	Cyt c <sup>79-88</sup>	KMIFVGIKKK	10	0.006	46
88	Cyt c <sup>4-13</sup>	EKGKKIFIMK	10	0.013	46
89	Cyt c <sup>5-13</sup>	KGKKIFIMK	9	0.069	46
90	MTS	AAVALLPAVLLALLAP	16	0.315	48
91	P14LRR	see fig. 1 reference 49	-	(7.958)	49
92	P11LRR	see fig. 1 reference 49	-	1.623	49, 50
93	(P10LRR-Gly) <sub>2</sub> -C5	see fig. 2 reference 50	-	(84.034)	50
94	(P10LRR-β-Ala) <sub>2</sub> -C5	see fig. 2 reference 50	-	(66.648)	50
95	(P10LRR-ABUA) <sub>2</sub> -C5	see fig. 2 reference 50	-	(73.892)	50
96	VPTLK	VPTLK	5	0.002	51
97	MAP(Aib)	KL(Aib)LKL(Aib)LK(Aib)LKA(Aib)LKL(Aib) <sup>1</sup>	18	(125.240)	52
98	sC18	GLRKRLRKFRNKIKEK	16	0.166	54
99	hCT(18-32)-k7	KKFKHTFPQTAIGVGAP KKRKAPKKKRKFA <sup>1</sup>	28	0.183	54, 57
100	N-E5L-hCT(18-32)-k7	GLLEALAELEKFKHTFPQTAIGVGAP KKRKAPKKKRKFA <sup>1</sup>	39	0.364	54
101	N-E5L-sC18	GLLEALAELEGLRKRLRKFRNKIKEK	27	0.150	54
102	N-E5L-Tat 48-60	GLLEALAELEGRKKRRQRRPPQ	24	0.507	54
103	FHV coat (35-49)	RRRRNRTRRRRRVR	15	(4.127)	56
104	PasTat	FFLIPKGGRRRRQRRPPQ	20	(4.426)	55
105	BMV Gag (7-25)	KMTRAQRRAAARRNRWTAR	19	0.288	56
106	HTLV-II Rex (4-16)	TRRQTRRRARRNR	13	0.288	56
107	Human cJun (252-279)	RIKAERKMRNRRIAASKSRKRKLERIAR	28	2.744	56
108	Human cFos (139-164)	KRRIRRRNKMAAAKSRNRRLTDT	26	0.199	56
109	K-FGF (Kaposi fibroblast growth factor)	AAVLLPVLLAAP	12	0.200	58
110	PreS2-TLM (PreS2-derived translocatory motif)	PLSSIFSRIGDP	12	0.224	58
111	PTD4 (Protein transduction domain 4)	PIRRRKKLRLK	12	0.658	58
112	α-peptide/β-peptoid chimera 2	see fig. 1 reference 59	-	0.185	59
113	α-peptide/β-peptoid chimera 6	see fig. 1 reference 59	-	2.040	59
114	α-peptide/β-peptoid chimera 8	see fig. 1 reference 59	-	2.102	59
115	hArg <sub>8</sub> (Homoarginine <sub>8</sub> )	see fig. 1 reference 59	-	0.464	59
116	PenArg	RQIRIWFQNRMRWR	16	1.810	60
117	PenLys	KQIKIWFQNKMKWK	16	0.041	60

118	aca-[Lys(Nys <sup>+</sup> )-aca] <sub>4</sub> -Lys(Nys <sup>+</sup> )	aca-[Lys(Nys <sup>+</sup> )-aca] <sub>4</sub> -Lys(Nys <sup>+</sup> ) <sup>2</sup>	-	0.001	61
119	aca-[Lys(Nys <sup>+</sup> )-aca] <sub>6</sub> -Lys(Nys <sup>+</sup> )	aca-[Lys(Nys <sup>+</sup> )-aca] <sub>6</sub> -Lys(Nys <sup>+</sup> ) <sup>2</sup>	-	0.005	61
120	M511	FLGKKFKKYFLQLLK	15	0.599	62
121	M551	KGKFLYLKLFKFL	15	0.240	62
122	G53-1	IVIAKLANLMCKTCRLAK	19	0.150	62
123	G53-2	AIGVNYLVKFIKVIKIAKLA	23	0.839	62
124	<i>Kno ref. 63</i> <i>(Knotted-1 homeodomain third helix)</i>	<i>KQIKINWFIQRRHWK</i>	18	(7.358)	63
125	R6/W3	RRWWRWR	9	0.910	63
126	Phe <sup>6,14</sup> -penetratin	RQKIFFQNRMMKFKK	16	0.727	64
127	Dodeca-penetratin	RQKIWFQNRMMKFKK	12	1.154	64
128	MG2d (Magainin 2 analogue)	GIGKFLHSAKKWKAFVGGQIMNC	23	0.798	65
129	BF2d (Buforin 2 analogue)	TRSSRAGLQWPVGRVHRLLRKGGC	24	0.953	65
130	YTA2	YTAIAWVKAFIRKLRK	16	1.545	66
131	K9	KKKKKKKKK	9	0.119	12
132	H9	HHHHHHHHH	9	0.068	12
133	O9	OOOOOOOOO	9	0.068	12
134	R8	RRRRRRRR	8	0.639	12, 16
135	R6	RRRRRR	6	0.194	12, 16
136	R5	RRRRR	5	0.077	12, 16
137	R4	RRRR	4	0.074	12
138	R3	RRR	3	0.055	12
139	D-R8	rrrrrrrr	8	1.577	12
140	D-R7	rrrrrr	7	1.071	12
141	D-R6	rrrrr	6	0.323	12
142	D-R5	rrrr	5	0.115	12
143	D-R4	rrrr	4	0.098	12
144	R15	RRRRRRRRRRRRRR	15	1.345	12
145	R20	RRRRRRRRRRRRRRRRRR	20	0.764	12
146	R25	RRRRRRRRRRRRRRRRRRRRRR	25	0.400	12
147	R30	RRRRRRRRRRRRRRRRRRRRRRRR	30	0.109	12
148	[Ala <sub>1</sub> ]pVEC	ALIILRRRIRKQAHAHSK	18	0.304	7
149	[Ala <sub>2</sub> ]pVEC	LAILRRRIRKQAHAHSK	18	0.507	7
150	[Ala <sub>3</sub> ]pVEC	LLAILRRRIRKQAHAHSK	18	0.406	7
151	[Ala <sub>4</sub> ]pVEC	LLIALRRRIRKQAHAHSK	18	0.659	7
152	[Ala <sub>5</sub> ]pVEC	LLIARRRIRKQAHAHSK	18	0.456	7
153	[Ala <sub>6</sub> ]pVEC	LLIILARRIRKQAHAHSK	18	2.433	7
154	[Ala <sub>7</sub> ]pVEC	LLIILRARIRKQAHAHSK	18	1.115	7
155	[Ala <sub>8</sub> ]pVEC	LLIILRRAIRKQAHAHSK	18	2.129	7
156	[Ala <sub>9</sub> ]pVEC	LLIILRRRARKQAHAHSK	18	0.760	7
157	[Ala <sub>10</sub> ]pVEC	LLIILRRRIAKQAHAHSK	18	1.470	7
158	[Ala <sub>11</sub> ]pVEC	LLIILRRRIRAKQAHAHSK	18	1.774	7
159	[Ala <sub>12</sub> ]pVEC	LLIILRRRIRKAAAHASK	18	1.420	7
160	[D-Ala <sub>13</sub> ]pVEC	LLIILRRRIRKQAAHASK	18	1.825	7
161	[Ala <sub>14</sub> ]pVEC	LLIILRRRIRKQAAAHASK	18	0.558	7
162	[D-Ala <sub>15</sub> ]pVEC	LLIILRRRIRKQAAHASK	18	1.115	7
163	[Ala <sub>16</sub> ]pVEC	LLIILRRRIRKQAAHASK	18	1.521	7
164	[Ala <sub>17</sub> ]pVEC	LLIILRRRIRKQAAHAAK	18	2.129	7
165	[Ala <sub>18</sub> ]pVEC	LLIILRRRIRKQAAHASK	18	2.079	7
166	retro-pVEC	KSHAHQKRIRRLILL	18	0.406	7
167	Ap1	AQIKIWFQNRMMKWKK	16	0.289	9
168	Ap2	RAIKIWFQNRMMKWKK	16	1.333	9
169	Ap3	RQAKIWFQNRMMKWKK	16	0.111	9
170	Ap4	RQAIWFQNRMMKWKK	16	0.511	9
171	Ap5	RQIKAWFQNRMMKWKK	16	0.244	9
172	Ap6	RQIKIAFQNRMMKWKK	16	0.222	9
173	Ap7	RQIKIWAQNRMMKWKK	16	0.089	9
174	Ap8	RQIKIWFANRRMMKWKK	16	0.778	9
175	Ap9	RQIKIWFQARRMMKWKK	16	0.978	9
176	Ap10	RQIKIWFQNRMMKWKK	16	0.400	9
177	Ap11	RQIKIWFQNRMMKWKK	16	0.242	9
178	Ap12	RQIKIWFQNRRAKWKK	16	0.644	9
179	Ap13	RQIKIWFQNRMMAWKK	16	0.378	9
180	Ap14	RQIKIWFQNRMMKAKK	16	0.356	9
181	Ap15	RQIKIWFQNRMMKWKK	16	0.411	9
182	Ap16	RQIKIWFQNRMMKWKKA	16	0.444	9
183	SAP (E)	VELPPPVELPPPVELPPP	18	0.007	67

184	Eng (Engrailed-2 homeodomain third helix)	SQIKIWFQNKRAKIKK	16	1.235	69
185	Hox (HoxA-13 homeodomain third helix)	RQVTIWFQNRrvKEKK	16	0.500	69
<i>186</i>	<i>Kno ref. 69</i> <i>(Knotted-1 homeodomain third helix)</i>	<i>KQINNWFINQRKRHWK</i>	<i>16</i>	<i>(11.118)</i>	<i>69</i>

*Peptides whose unified response is an outlier are indicated in italic. Their unreliable CP-responses were not considered during data-evaluation.*

<sup>1</sup>Aib = alpha amino-isobutyric acid

<sup>2</sup>Aca = NH<sub>2</sub>(CH<sub>2</sub>)<sub>5</sub>CO-; Lys(Nys<sup>+</sup>) = Redox amino acid = Lys with 1,4-dihydrotriognelline side chain